

SEQ ID NO 89

LENGTH: 775

TYPE: PRT

ORGANISM: Pyrococcus furiosus

SEQUENCE: 89

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp **Val** Pro Thr Ile
85 90 95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125
Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr

	420		425		430										
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly
	435				440							445			
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile
	450				455							460			
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu
	465				470							475			480
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly
					485							490			495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu
					500							505			510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Lys	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu
					515							520			525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly
					530							535			540
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Ser	Glu	Glu	Ile	Lys	Lys	Lys
	545					550						555			560
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu
					565							570			575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys
					580							585			590
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly
					595							600			605
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln
					610							615			620
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala
					625							630			640
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile
						645						650			655
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His
						660						665			670
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala
					675							680			685
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val
					690							695			700
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu
					705							710			720
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn
						725						730			735
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg
						740						745			750
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser
					755							760			765
Trp	Leu	Asn	Ile	Lys	Lys	Ser									
					770							775			

Examiner's alignment::

BRS	L1	63480	polymerase	USPAT	2010/09/29 14:05
BRS	L2	24	11 and v93	USPAT	2010/09/29 14:05
BRS	L3	38105	11 and (valine mutation)	USPAT	2010/09/29 14:14
BRS	L4	744	11 and (valine.clm.)	USPAT	2010/09/29 14:14
BRS	L5	30	14 and polymerase.clm.	USPAT	2010/09/29 14:15
BRS	L6	40	valine adj mutation	USPAT	2010/09/29 14:28
BRS	L7	187	(valine adj mutation) or (valine adj substitution)	USPAT	
		2010/09/29 14:28			

BRS	L8	139	11 and 17	USPAT	2010/09/29 14:29
BRS	L9	9	18 and polymerase .clm.	USPAT	2010/09/29 14:29
BRS	L10	11437	11 and uracil	USPAT	2010/09/29 14:37
BRS	L11	1197	110 and polymerase.clm.	USPAT	2010/09/29 14:37
BRS	L12	9	15 and uracil	USPAT	2010/09/29 14:38

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:53:01 ON 29 SEP 2010)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, JAPIO, BIOTECHNO' ENTERED AT

14:54:04 ON 29 SEP 2010

L1	1669300 S POLYMERASE
L2	1 S L1 AND V93
L3	5269 S L1 AND URACIL
L4	1 S L1 AND POLYMERASE.TI.
L5	5057 S L1 AND VALINE
L6	13 S L5 AND URACIL
L7	11 DUP REM L6 (2 DUPLICATES REMOVED)
L8	11938 S L1 AND EXONUCLEASE
L9	29 S L8 AND VALINE
L10	14 DUP REM L9 (15 DUPLICATES REMOVED)

ANSWER 10 OF 14 CAPLUS COPYRIGHT 2010 ACS on STN

AN 1999:409781 CAPLUS

DN 131:225462

TI A Single Tyrosine Prevents Insertion of Ribonucleotides in the Eukaryotic-type .phi.29 DNA Polymerase

AU Bonnin, Ana; Lazaro, Jose M.; Blanco, Luis; Salas, Margarita

CS Centro de Biologia Molecular "Severo Ochoa" (CSIC-UAM), Universidad Autonoma, Canto Blanco, Madrid, 28049, Spain

SO Journal of Molecular Biology (1999), 290(1), 241-251

CODEN: JMOBAK; ISSN: 0022-2836

PB Academic Press

DT Journal

LA English

AB Three conserved motifs (named A, B and C) have been proposed to form the polynn. active site in all classes of DNA-dependent polymerases. In eukaryotic-type (.alpha.-like) DNA polymerases, motif A is characterized by the consensus "Dx2SLYP". Mutants in .phi.29 DNA polymerase residue Tyr254 of this conserved motif had been previously shown to be affected in dNTP binding. Here, we show that a single substitution of Tyr254 into a valine residue enables the enzyme to incorporate ribonucleotide substrates, without affecting its wild-type affinity for dNTPs. Whereas the wild-type enzyme preferred dNTPs more than two million-fold over rNTPs, the mutation of Tyr254 into valine reduced the discrimination for rNTPs up to 1000-fold. In addn. to this discrimination mechanism, based on sugar selection, .phi.29 DNA polymerase is very inefficient when extending an RNA primer terminus, allowing its exonucleolytic degrdn. These results indicate that the Tyr254 of .phi.29 DNA polymerase is responsible for the discrimination against the 2'-OH group of an incoming ribonucleotide. This is the first time that the invariant tyrosine residue of motif A is

involved in ribo- vs. deoxyribonucleotide discrimination in an eukaryotic-type DNA polymerase. (c) 1999 Academic Press.

OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

SEQ ID NO 108

LENGTH: 882

TYPE: PRT

ORGANISM: *Sulfolobus solfataricus*

SEQUENCE: 108

Met	Thr	Lys	Gln	Leu	Thr	Leu	Phe	Asp	Ile	Pro	Ser	Ser	Lys	Pro	Ala
1									5		10				15
Lys	Ser	Glu	Gln	Asn	Thr	Gln	Gln	Ser	Gln	Gln	Ser	Ala	Pro	Val	Glu
									20		25				30
Glu	Lys	Lys	Val	Val	Arg	Arg	Glu	Trp	Leu	Glu	Glu	Ala	Gln	Glu	Asn
									35		40				45
Lys	Ile	Tyr	Phe	Leu	Leu	Gln	Val	Asp	Tyr	Asp	Gly	Lys	Lys	Gly	Lys
									50		55				60
Ala	Val	Cys	Lys	Leu	Phe	Asp	Lys	Glu	Thr	Gln	Lys	Ile	Tyr	Ala	Leu
									65		70				75
Tyr	Asp	Asn	Thr	Gly	His	Lys	<u>Pro</u>	<u>Tyr</u>	<u>Phe</u>	<u>Leu</u>	Val	Asp	Leu	Glu	Pro
									85		90				95
Asp	Lys	Val	Gly	Lys	Ile	Pro	Lys	Ile	Val	Arg	Asp	Pro	Ser	Phe	Asp
					100				105						110
His	Ile	Glu	Thr	Val	Ser	Lys	Ile	Asp	Pro	Tyr	Thr	Trp	Asn	Lys	Phe
									115		120				125
Lys	Leu	Thr	Lys	Ile	Val	Val	Arg	Asp	Pro	Leu	Ala	Val	Arg	Arg	Leu
									130		135				140
Arg	Asn	Asp	Val	Pro	Lys	Ala	Tyr	Glu	Ala	His	Ile	Lys	Tyr	Phe	Asn
									145		150				155
Asn	Tyr	Met	Tyr	Asp	Ile	Gly	Leu	Ile	Pro	Gly	Met	Pro	Tyr	Val	Val
									165		170				175
Lys	Asn	Gly	Lys	Leu	Glu	Ser	Val	Tyr	Leu	Ser	Leu	Asp	Glu	Lys	Asp
									180		185				190
Val	Glu	Glu	Ile	Lys	Lys	Ala	Phe	Ala	Asp	Ser	Asp	Glu	Met	Thr	Arg
									195		200				205
Gln	Met	Ala	Val	Asp	Trp	Leu	Pro	Ile	Phe	Glu	Thr	Glu	Ile	Pro	Lys
									210		215				220
Ile	Lys	Arg	Val	Ala	Ile	Asp	Ile	Glu	Val	Tyr	Thr	Pro	Val	Lys	Gly
									225		230				240
Arg	Ile	Pro	Asp	Ser	Gln	Lys	Ala	Glu	Phe	Pro	Ile	Ile	Ser	Ile	Ala
									245		250				255
Leu	Ala	Gly	Ser	Asp	Gly	Leu	Lys	Lys	Val	Leu	Val	Leu	Asn	Arg	Asn
									260		265				270
Asp	Val	Asn	Glu	Gly	Ser	Val	Lys	Leu	Asp	Gly	Ile	Ser	Val	Glu	Arg
									275		280				285
Phe	Asn	Thr	Glu	Tyr	Glu	Leu	Leu	Gly	Arg	Phe	Phe	Asp	Ile	Leu	Leu
									290		295				300
Glu	Tyr	Pro	Ile	Val	Leu	Thr	Phe	Asn	Gly	Asp	Asp	Phe	Asp	Leu	Pro
									305		310				320
Tyr	Ile	Tyr	Phe	Arg	Ala	Leu	Lys	Leu	Gly	Tyr	Phe	Pro	Glu	Glu	Ile
									325		330				335
Pro	Ile	Asp	Val	Ala	Gly	Lys	Asp	Glu	Ala	Lys	Tyr	Leu	Ala	Gly	Leu
									340		345				350
His	Ile	Asp	Leu	Tyr	Lys	Phe	Phe	Asn	Lys	Ala	Val	Arg	Asn	Tyr	
									355		360				365
Ala	Phe	Glu	Gly	Lys	Tyr	Asn	Glu	Tyr	Asn	Leu	Asp	Ala	Val	Ala	Lys
									370		375				380
Ala	Leu	Leu	Gly	Thr	Ser	Lys	Val	Lys	Val	Asp	Thr	Leu	Ile	Ser	Phe
									385		390				400
Leu	Asp	Val	Glu	Lys	Leu	Ile	Glu	Tyr	Asn	Phe	Arg	Asp	Ala	Glu	Ile
									405		410				415
Thr	Leu	Gln	Leu	Thr	Thr	Phe	Asn	Asn	Asp	Leu	Thr	Met	Lys	Leu	Ile

420	425	430
Val Leu Phe Ser Arg Ile Ser Arg	Leu Gly Ile Glu Glu	Leu Thr Arg
435	440	445
Thr Glu Ile Ser Thr Trp Val Lys Asn Leu Tyr Tyr	Trp Glu His Arg	
450	455	460
Lys Arg Asn Trp Leu Ile Pro Leu Lys Glu Glu	Ile Leu Ala Lys Ser	
465	470	475
Ser Asn Ile Arg Thr Ser Ala Leu Ile Lys Gly Lys	Gly Tyr Lys Gly	
485	490	495
Ala Val Val Ile Asp Pro Pro Ala Gly Ile Phe Phe Asn	Ile Thr Val	
500	505	510
Leu Asp Phe Ala Ser Leu Tyr Pro Ser Ile Ile Arg Thr	Trp Asn Leu	
515	520	525
Ser Tyr Glu Thr Val Asp Ile Gln Gln Cys Lys Lys	Pro Tyr Glu Val	
530	535	540
Lys Asp Glu Thr Gly Glu Val Leu His Ile Val Cys Met	Asp Arg Pro	
545	550	555
Gly Ile Thr Ala Val Ile Thr Gly Leu Leu Arg Asp Phe	Arg Val Lys	
565	570	575
Ile Tyr Lys Lys Ala Lys Asn Pro Asn Asn Ser	Glu Gln Lys	
580	585	590
Leu Leu Tyr Asp Val Val Gln Arg Ala Met Lys Val Phe	Ile Asn Ala	
595	600	605
Thr Tyr Gly Val Phe Gly Ala Glu Thr Phe Pro	Leu Tyr Ala Pro Ala	
610	615	620
Val Ala Glu Ser Val Thr Ala Leu Gly Arg Tyr Val	Ile Thr Ser Thr	
625	630	635
Val Lys Lys Ala Arg Glu Glu Gly Leu Thr Val Leu	Tyr Gly Asp Thr	
645	650	655
Asp Ser Leu Phe Leu Leu Asn Pro Pro Lys Asn Ser	Leu Glu Asn Ile	
660	665	670
Ile Lys Trp Val Lys Thr Thr Phe Asn Leu Asp Leu	Glu Val Asp Lys	
675	680	685
Thr Tyr Lys Phe Val Ala Phe Ser Gly Leu Lys Lys	Asn Tyr Phe Gly	
690	695	700
Val Tyr Gln Asp Gly Lys Val Asp Ile Lys Gly Met	Leu Val Lys Lys	
705	710	715
Arg Asn Thr Pro Glu Phe Val Lys Lys Val Phe Asn	Glu Val Lys Glu	
725	730	735
Leu Met Ile Ser Ile Asn Ser Pro Asn Asp Val Lys	Glu Ile Lys Arg	
740	745	750
Lys Ile Val Asp Val Val Lys Gly Ser Tyr Glu Lys	Leu Lys Asn Lys	
755	760	765
Gly Tyr Asn Leu Asp Glu Leu Ala Phe Lys Val Met	Leu Ser Lys Pro	
770	775	780
Leu Asp Ala Tyr Lys Lys Asn Thr Pro Gln His Val	Lys Ala Ala Leu	
785	790	795
Gln Leu Arg Pro Phe Gly Val Asn Val Leu Pro Arg	Asp Ile Ile Tyr	
805	810	815
Tyr Val Lys Val Arg Ser Lys Asp Gly Val Lys Pro	Val Gln Leu Ala	
820	825	830
Lys Val Thr Glu Ile Asp Ala Glu Lys Tyr Leu Glu	Ala Leu Arg Ser	
835	840	845
Thr Phe Glu Gln Ile Leu Arg Ala Phe Gly Val Ser	Trp Asp Glu Ile	
850	855	860
Ala Ala Thr Met Ser Ile Asp Ser Phe Phe Ser	Tyr Pro Ser Lys Gly	
865	870	875
Asn Ser		880